

## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- 5 (i) APPLICANT: Michael A. Apicella  
Melvin G. Sunshine  
Na-Gyong Lee  
Bradley Gibson  
Rasappa Arumugham
- 10 (ii) TITLE OF INVENTION: Non-Toxic Mutants of Pathogenic  
Gram-Negative Bacteria
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Hodgson, Russ, Andrews, Woods &  
Goodyear
- (B) STREET: 1800 One M&T Plaza
- (C) CITY: Buffalo
- (D) STATE: New York
- 20 (E) COUNTRY: United States
- (F) ZIP: 14203-2391
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb  
storage
- 25 (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
3.1
- (D) SOFTWARE: Wordperfect for Windows 5.1
- (vi) APPLICATION DATA:
- 30 (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (vii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Nelson, M. Bud
- (B) REGISTRATION NUMBER: 35,300
- 35 (C) REFERENCE DOCKET NUMBER: 22244.0002
- (viii) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (716) 856-4000
- (B) TELEFAX: (716) 849-0349
- 40 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 969 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double-stranded
- 45 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: yes
- (iv) ORIGINAL SOURCE:
- (A) ORGANISM: *H. influenzae*
- 50 (B) STRAIN: 2019
- (C) CELL TYPE: bacterium
- (v) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAAACTACGC CCCTAACTTA CGTGGAAAGA ACA ATG AAA AAC 42

Met Lys Asn  
1

5	GAA	AAA	CTC	CCT	CAA	TTT	CAA	CCG	CAC	TTT	TTA	GCC	CCA	81
	Glu	Lys	Leu	Pro	Gln	Phe	Gln	Pro	His	Phe	Leu	Ala	Pro	
		5					10					15		
10	AAA	TAC	TGG	CTT	TTT	TGG	CTA	GGC	GTG	GCA	ATT	TGG	CGA	120
	Lys	Tyr	Trp	Leu	Phe	Trp	Leu	Gly	Val	Ala	Ile	Trp	Arg	
			20						25					
15	AGT	ATT	TTA	TGT	CTT	CCC	TAT	CCT	ATT	TTG	CGC	CAT	ATT	159
	Ser	Ile	Leu	Cys	Leu	Pro	Tyr	Pro	Ile	Leu	Arg	His	Ile	
	30					35					40			
20	GGT	CAT	GGT	TTC	GGT	TGG	CTG	TTT	TCA	CAT	TTA	AAA	GTG	198
	Gly	His	Gly	Phe	Gly	Trp	Leu	Phe	Ser	His	Leu	Lys	Val	
			45					50					55	
25	GGT	AAA	CGT	CGA	GCT	GCC	ATT	GCA	CGC	CGT	AAT	CTT	GAA	237
	Gly	Lys	Arg	Arg	Ala	Ala	Ile	Ala	Arg	Arg	Asn	Leu	Glu	
					60					65				
30	CTT	TGT	TTC	CCT	GAT	ATG	CCT	GAA	AAC	GAA	CGT	GAG	ACG	276
	Leu	Cys	Phe	Pro	Asp	Met	Pro	Glu	Asn	Glu	Arg	Glu	Thr	
		70					75					80		
35	ATT	TTG	CAA	GAA	AAT	CTT	CGT	TCA	GTA	GGC	ATG	GCA	ATT	315
	Ile	Leu	Gln	Glu	Asn	Leu	Arg	Ser	Val	Gly	Met	Ala	Ile	
				85					90				95	
40	ATC	GAA	ACT	GGC	ATG	GCT	TGG	TTT	TGG	TCG	GAT	TCA	CGT	354
	Ile	Glu	Thr	Gly	Met	Ala	Trp	Phe	Trp	Ser	Asp	Ser	Arg	
					100						105			
45	ATC	AAA	AAA	TGG	TCG	AAA	GTT	GAA	GGC	TTA	CAT	TAT	CTA	393
	Ile	Lys	Lys	Trp	Ser	Lys	Val	Glu	Gly	Leu	His	Tyr	Leu	
			110					115					120	
50	AAA	GAA	AAT	CAA	AAA	GAT	GGA	ATT	GTT	CTC	GTC	GGC	GTT	432
	Lys	Glu	Asn	Gln	Lys	Asp	Gly	Ile	Val	Leu	Val	Gly	Val	
					125					130				
55	CAT	TTC	TTA	ACG	CTA	GAA	CTT	GGC	GCA	CGC	ATC	ATT	GGT	471
	His	Phe	Leu	Thr	Leu	Glu	Leu	Gly	Ala	Arg	Ile	Ile	Gly	
		135					140					145		
60	TTA	CAT	CAT	CCT	GGC	ATT	GGT	GTT	TAT	CGT	CCA	AAT	GAT	510
	Leu	His	His	Pro	Gly	Ile	Gly	Val	Tyr	Arg	Pro	Asn	Asp	
				150					155					
65	AAT	CCT	TTG	CTT	GAT	TGG	CTA	CAA	ACA	CAA	GGC	CGT	TTA	549
	Asn	Pro	Leu	Pro	Asp	Trp	Leu	Gln	Thr	Gln	Gly	Arg	Leu	
	160					165					170			

364407 254060

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CGC TCC AAT AAA GAT ATG CTT GAT CGT AAA GAT TTA CGC 588  
Arg Ser Asn Lys Asp Met Leu Asp Arg Lys Asp Leu Arg  
175 180 185

5 GGA ATG ATC AAA GCT TTA CGC CAC GAA GAA ACC ATT TGG 627  
Gly Met Ile Lys Ala Leu Arg His Glu Glu Thr Ile Trp  
190 195

10 TAT GCG CCT GAT CAC GAT TAC GGC AGA AAA AAT GCC GTT 666  
Tyr Ala Pro Asp His Asp Tyr Gly Arg Lys Asn Ala Val  
200 205 210

15 TTT GTT CCT TTT TTT GCA GTA CCT GAC ACT TGC ACT ACT 705  
Phe Val Pro Phe Phe Ala Val Pro Asp Thr Cys Thr Thr  
215 220

20 ACT GGT AGT TAT TAT TTA TTG AAA TCC TCG CAA AAC AGC 744  
Thr Gly Ser Tyr Tyr Leu Leu Lys Ser Ser Gln Asn Ser  
225 230 235

AAA GTG ATT CCA TTT GCG CCA TTA CGC AAT AAA GAT GGT 783  
Lys Val Ile Pro Phe Ala Pro Leu Arg Asn Lys Asp Gly  
240 245 250

25 TCA GGC TAT ACC GTG AGC ATT TCA GCG CCT GTT GAT TTT 822  
Ser Gly Tyr Thr Val Ser Ile Ser Ala Pro Val Asp Phe  
255 260

30 ACA GAT TTA CAA GAT GAA GTA GCG ATA GCT GTG CGA ATG 861  
Thr Asp Leu Gln Asp Glu Val Ala Ile Ala Val Arg Met  
265 270 275

35 AAT CAA ATC GTT GAA AAG GAA ATC ATG AAG GGC ATA TCA 900  
Asn Gln Ile Val Glu Lys Glu Ile Met Lys Gly Ile Ser  
280 285

CAA TAT ATG TGG CTA CAT CGT CGT TTT AAA ACA CGC CCC  
Gln Tyr Met Trp Leu His Arg Arg Phe Lys Thr Arg Pro  
290 295 300

40 GAT GAA AAT ACG CCT AGT TTA TAC GAT TAA 969  
Asp Glu Asn Thr Pro Ser Leu Tyr Asp  
305 310

45

## (3) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 nucleotides  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single-stranded  
(D) TOPOLOGY: linear

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## (ii) ORIGINAL SOURCE:

- (A) ORGANISM: *H. influenzae*  
(B) STRAIN: 2019

- (iii) IMMEDIATE SOURCE: synthesized  
(iv) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCAATATGGC GCAAAATAGG ATAGGGAAGA C 31

5

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 nucleotides  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: single-stranded  
(D) TOPOLOGY: linear

(ii) ORIGINAL SOURCE:

- (A) ORGANISM: *H. influenzae*

(iii) FEATURE:

- 15 (A) OTHER INFORMATION: uptake sequence for transformation

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGTGCGGT 9

20

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 nucleotides  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: single-stranded  
(D) TOPOLOGY: linear

(ii) FEATURE:

- (A) OTHER INFORMATION: hybridizes to TNF $\alpha$  mRNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30

ATCTCTCAGC TCCACGCCAT TGGCCAGGAG 30

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 nucleotides  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single-stranded  
(D) TOPOLOGY: linear

(ii) FEATURE:

- 40 (A) OTHER INFORMATION: does not hybridize to TNF $\alpha$  mRNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCCTGGCCA ATGGCGTGGA GCTGAGAGAT 30